RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _/0/522,389_

Source: _PU_

Date Processed by STIC: _1/26/06_

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PCT

RAW SEQUENCE LISTING   DATE: 01/26/2006
PATENT APPLICATION: US/10/522,389   TIME: 09:19:40

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Output Set: N:\CRF4\01262006\J522389.raw

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 3 <110> APPLICANT: PEL, Herman J.
 4        HOPPER, Sylvia
 6 <120> TITLE OF INVENTION: GENES FROM PROPIONIBACTERIUM FREUDENREICHII
 7        ENCODING ENZYMES INVOLVED IN VITAMIN B12 BIOSYNTHESIS
 9 <130> FILE REFERENCE: 246152024900
11 <140> CURRENT APPLICATION NUMBER: US 10/522,389
C--> 12 <141> CURRENT FILING DATE: 2005-01-25
14 <150> PRIOR APPLICATION NUMBER: PCT/EP03/008216
15 <151> PRIOR FILING DATE: 2003-07-25
17 <150> PRIOR APPLICATION NUMBER: EP 02255203.8
18 <151> PRIOR FILING DATE: 2002-07-25
20 <160> NUMBER OF SEQ ID NOS: 17
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2586
26 <212> TYPE: DNA
27 <213> ORGANISM: Propionibacterium freudenreichii
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(2586)
32 <223> OTHER INFORMATION:
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39 tcc agc cag gga aag acc acc gtg gcc atc ggc ctg atg gcg gcc ctg     96
40 Ser Ser Gln Gly Lys Thr Thr Val Ala Ile Gly Leu Met Ala Ala Leu
41              20                  25                  30
43 cgg gcc tcg ggg cgc agc gtg gcc gga ttc aag gtg ggc ccc gac tac    144
44 Arg Ala Ser Gly Arg Ser Val Ala Gly Phe Lys Val Gly Pro Asp Tyr
45          35                  40                  45
47 atc gat ccg ggc tat cac gca ctg gcc tgc ggt cgc ccc ggc cgc aac    192
48 Ile Asp Pro Gly Tyr His Ala Leu Ala Cys Gly Arg Pro Gly Arg Asn
49      50                  55                  60
51 ctg gat ccc tat ttg tgc ggg ccc gag cgc att gcg ccg ttg ttc gcc    240
52 Leu Asp Pro Tyr Leu Cys Gly Pro Glu Arg Ile Ala Pro Leu Phe Ala
53 65                  70                  75                  80
55 cat ggc gcg ctg cat ccc gaa ccc gcg gac atc tcg gtc gtc gaa ggc    288
56 His Gly Ala Leu His Pro Glu Pro Ala Asp Ile Ser Val Val Glu Gly
57              85                  90                  95
59 gtg atg ggc atg ttc gac ggc aag ctc ggc gcg tgg ccc gac ggc acc    336
60 Val Met Gly Met Phe Asp Gly Lys Leu Gly Ala Trp Pro Asp Gly Thr
61              100                 105                 110
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 63 gat gac ccc gcc ggt ttt ggc tca tcg gcc cat atc gcc agg ctg ctc    384
 64 Asp Asp Pro Ala Gly Phe Gly Ser Ser Ala His Ile Ala Arg Leu Leu
 65         115                 120                 125
 67 gat gcc ccc gtg ctg ctc gtg gtc gac ggc tca cac agt gcc cgt acc    432
 68 Asp Ala Pro Val Leu Leu Val Val Asp Gly Ser His Ser Ala Arg Thr
 69         130                 135                 140
 71 gcc gca gcc ctg tgc cat ggc ctg gcc agc tac gat ccc cgc atc cat    480
 72 Ala Ala Ala Leu Cys His Gly Leu Ala Ser Tyr Asp Pro Arg Ile His
 73 145                 150                 155                 160
 75 gtg gcc ggc gtc atc ctc aat cgg gtg atg ggt gcc cgc gtg gtc gac    528
 76 Val Ala Gly Val Ile Leu Asn Arg Val Met Gly Ala Arg Val Val Asp
 77                 165                 170                 175
 79 gag atc acc cgg ggc tgc gca cgt gtc ggc ctg ccg gtg ctg ggg gct    576
 80 Glu Ile Thr Arg Gly Cys Ala Arg Val Gly Leu Pro Val Leu Gly Ala
 81         180                 185                 190
 83 ctg ccg aaa agc acg cgg gtg gcc gtg ggc tca cgc cac ctg gga ctg    624
 84 Leu Pro Lys Ser Thr Arg Val Ala Val Gly Ser Arg His Leu Gly Leu
 85         195                 200                 205
 87 gtc acg gcc gac gag cag ggt gac gcg atc ggc atc gtg cag cag gcc    672
 88 Val Thr Ala Asp Glu Gln Gly Asp Ala Ile Gly Ile Val Gln Gln Ala
 89         210                 215                 220
 91 ggt gag ctc gtc gcc gca cac ctc gac ctc gac gcc atc gcc acg atc    720
 92 Gly Glu Leu Val Ala Ala His Leu Asp Leu Asp Ala Ile Ala Thr Ile
 93 225                 230                 235                 240
 95 gcc ggt ggg gcc cct gac ctg gcc gtc gat ccc tgg gat ccc gcc gca    768
 96 Ala Gly Gly Ala Pro Asp Leu Ala Val Asp Pro Trp Asp Pro Ala Ala
 97                 245                 250                 255
 99 gag gtc gaa ccg gta ccg ggg cgt ccg gtc atc gcc atg gcc tcg ggt    816
100 Glu Val Glu Pro Val Pro Gly Arg Pro Val Ile Ala Met Ala Ser Gly
101                 260                 265                 270
103 ccc gca ttc acc ttc cgg tac acc gaa acc gca gaa ctg ctg gag gcg    864
104 Pro Ala Phe Thr Phe Arg Tyr Thr Glu Thr Ala Glu Leu Leu Glu Ala
105         275                 280                 285
107 gcc ggc tgc cgg gtg acg gcc ttc gat ccg ctc acc gcc cgg ggc ctt    912
108 Ala Gly Cys Arg Val Thr Ala Phe Asp Pro Leu Thr Ala Arg Gly Leu
109         290                 295                 300
111 ccg gcc gat gtg tcc ggc ctg tac ctg ggg ggt ggt ttc ccc gag gag    960
112 Pro Ala Asp Val Ser Gly Leu Tyr Leu Gly Gly Gly Phe Pro Glu Glu
113 305                 310                 315                 320
115 cac gcc gag gcg ctc gcc ggc aac acc tcc ctg ggc gct gaa atc gcc   1008
116 His Ala Glu Ala Leu Ala Gly Asn Thr Ser Leu Gly Ala Glu Ile Ala
117                 325                 330                 335
119 tca cgc gtg tcc gag ggc ctg ccg acg gtg gcc gag tgt gcg ggg ctg   1056
120 Ser Arg Val Ser Glu Gly Leu Pro Thr Val Ala Glu Cys Ala Gly Leu
121                 340                 345                 350
123 ctc tac ctg tgc cgc agc ctg gat gga ctg gcg atg gcc ggg gtg gtc   1104
124 Leu Tyr Leu Cys Arg Ser Leu Asp Gly Leu Ala Met Ala Gly Val Val
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127 gac gcc gac tcg tcc atg acg ccg cgc ctg acc atc ggc tac cac cac   1152
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128 Asp Ala Asp Ser Ser Met Thr Pro Arg Leu Thr Ile Gly Tyr His His
129     370                 375             380
131 gcc cgc gcc gcc aac gac agc ttc ctg atg cgc gcc ggg gag cgc tat   1200
132 Ala Arg Ala Ala Asn Asp Ser Phe Leu Met Arg Ala Gly Glu Arg Tyr
133 385             390             395                 400
135 cgg gcc cat gag ttc cac cgc acc acc ctg gac acg ccc ccc tac gac   1248
136 Arg Ala His Glu Phe His Arg Thr Thr Leu Asp Thr Pro Pro Tyr Asp
137             405                 410                 415
139 cgc gac ccc gga cca caa cgg ctg ggc gac caa cgg ttg gcg tgg gac   1296
140 Arg Asp Pro Gly Pro Gln Arg Leu Gly Asp Gln Arg Leu Ala Trp Asp
141             420                 425             430
143 gtg gag acc ccg acg ggg ggc aac cga ccc gag ggg gtg ctg gtc gcc   1344
144 Val Glu Thr Pro Thr Gly Gly Asn Arg Pro Glu Gly Val Leu Val Ala
145         435                 440                 445
147 ccg acc ccc ggt tcc gcg ccc agc gtc cac gcc tcc tac cag cac ctg   1392
148 Pro Thr Pro Gly Ser Ala Pro Ser Val His Ala Ser Tyr Gln His Leu
149         450                 455                 460
151 cac tgg gca ggg agt ccg gta ctg gcg caa cgc ttc gcc cgg gcg gcg   1440
152 His Trp Ala Gly Ser Pro Val Leu Ala Gln Arg Phe Ala Arg Ala Ala
153 465                 470                 475                 480
155 agc gaa tat ggg cac acc ggc cat cac tcc ccc cgg cct gcc gcc acg   1488
156 Ser Glu Tyr Gly His Thr Gly His His Ser Pro Arg Pro Ala Ala Thr
157             485                 490                 495
159 acg ccg gga gat gcg ttg tcc gca gcg ccc gac ctc acc cat cac ggg   1536
160 Thr Pro Gly Asp Ala Leu Ser Ala Ala Pro Asp Leu Thr His His Gly
161             500                 505                 510
163 gat cgc gat gtg ctg ccc ggc ctg gtc gac ttg gcg gtg aac gtg cgc   1584
164 Asp Arg Asp Val Leu Pro Gly Leu Val Asp Leu Ala Val Asn Val Arg
165             515                 520                 525
167 gat gtg cga cct ccg gcc tgg ctc gtg gag cgc atc gtc gcc tcc agc   1632
168 Asp Val Arg Pro Pro Ala Trp Leu Val Glu Arg Ile Val Ala Ser Ser
169     530                 535                 540
171 gac cag tgg gcc cac tac ccc gat cag cgc gaa gcg acc cgt gcg gtg   1680
172 Asp Gln Trp Ala His Tyr Pro Asp Gln Arg Glu Ala Thr Arg Ala Val
173 545                 550                 555                 560
175 gca ctg cgc cat ggc gtc aac ccc gac cag gta ctg ctc acg gcc ggg   1728
176 Ala Leu Arg His Gly Val Asn Pro Asp Gln Val Leu Leu Thr Ala Gly
177             565                 570                 575
179 tcc tcg gag gcg ttc agc ctg atc gcc cac ggg ttc tcc ccg cgc tgg   1776
180 Ser Ser Glu Ala Phe Ser Leu Ile Ala His Gly Phe Ser Pro Arg Trp
181             580                 585                 590
183 gcg gtc gtg gtg cat ccc cag ttc acc gaa cca gag gtg gcc ctg cgc   1824
184 Ala Val Val Val His Pro Gln Phe Thr Glu Pro Glu Val Ala Leu Arg
185         595                 600                 605
187 aac gcc ggg cgc ccg gtc ggc cgc ctg gtg ctc cat gcc tcg gat ggc   1872
188 Asn Ala Gly Arg Pro Val Gly Arg Leu Val Leu His Ala Ser Asp Gly
189     610                 615                 620
191 ttc cag ttc gat cac gaa ctg ctg gac ccc agg gcc gac atg gtg gtc   1920
192 Phe Gln Phe Asp His Glu Leu Leu Asp Pro Arg Ala Asp Met Val Val
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193 625                      630                  635                       640
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196 Ile Gly Asn Pro Thr Asn Pro Thr Gly Val Leu His Ser Ala Ala Ser
197             645                  650                  655
199 ctg cgc gcg ttg tgc cgg ccc gga cgc gtg gtg gtg gtt gac gag gca    2016
200 Leu Arg Ala Leu Cys Arg Pro Gly Arg Val Val Val Val Asp Glu Ala
201             660                  665                  670
203 ttc atg gac gcc gtg ccg ggc gag ccc gag agc ctc atc ggg gca cgc    2064
204 Phe Met Asp Ala Val Pro Gly Glu Pro Glu Ser Leu Ile Gly Ala Arg
205             675                  680                  685
207 atg gat ggc ctg ttg gtc acc cgc tcg ttc acg aag act tgg agc gtc    2112
208 Met Asp Gly Leu Leu Val Thr Arg Ser Phe Thr Lys Thr Trp Ser Val
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211 ccg ggg ctg cgg atc gga tat gtg gtc ggg gat ccc gcg ctc att cgc    2160
212 Pro Gly Leu Arg Ile Gly Tyr Val Val Gly Asp Pro Ala Leu Ile Arg
213 705                  710                  715                  720
215 gtc ctg gcg cac gaa cag ccc tgt tgg ccc atc tcc acc ccc gcc ctg    2208
216 Val Leu Ala His Glu Gln Pro Cys Trp Pro Ile Ser Thr Pro Ala Leu
217             725                  730                  735
219 gtc acc gcc cgc gaa tgc tcc acg cca cgc gcc gtg gag cag gcc acc    2256
220 Val Thr Ala Arg Glu Cys Ser Thr Pro Arg Ala Val Glu Gln Ala Thr
221             740                  745                  750
223 tca gat gcc cga cag gcg gcg cag gac cgc cga cac ctg gtg gcc cgc    2304
224 Ser Asp Ala Arg Gln Ala Ala Gln Asp Arg Arg His Leu Val Ala Arg
225             755                  760                  765
227 ctg gcc ggg atc ggc atc cag acc gtc ggg gag gcc agg gcc ccc ttc    2352
228 Leu Ala Gly Ile Gly Ile Gln Thr Val Gly Glu Ala Arg Ala Pro Phe
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231 gtc cta gtc gac ctg cgc gcc cac ccg ccc ggt ggg ctt cgt gcg gga    2400
232 Val Leu Val Asp Leu Arg Ala His Pro Pro Gly Gly Leu Arg Ala Gly
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235 ttg cgg acg ctc ggc ttc acc gtg cgc agc ggc gag agc ttc ccc ggc    2448
236 Leu Arg Thr Leu Gly Phe Thr Val Arg Ser Gly Glu Ser Phe Pro Gly
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239 ctg ggc gcg ggc tgg ttg cgg ctc gcg gtt cgc cac ccg gac atc agc    2496
240 Leu Gly Ala Gly Trp Leu Arg Leu Ala Val Arg His Pro Asp Ile Ser
241             820                  825                  830
243 gac gcg ttc gtc gct gcc ctg gcc cgc acc atc gac gca ctg gac aca    2544
244 Asp Ala Phe Val Ala Ala Leu Ala Arg Thr Ile Asp Ala Leu Asp Thr
245             835                  840                  845
247 gcg cag cac ccc atg cga cca cca caa gga gac atc aga tga           2586
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249     850                  855                  860
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253 <211> LENGTH: 861
254 <212> TYPE: PRT
255 <213> ORGANISM: Propionibacterium freudenreichii
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264 Arg Ala Ser Gly Arg Ser Val Ala Gly Phe Lys Val Gly Pro Asp Tyr
265         35                  40                  45
267 Ile Asp Pro Gly Tyr His Ala Leu Ala Cys Gly Arg Pro Gly Arg Asn
268         50                  55                  60
270 Leu Asp Pro Tyr Leu Cys Gly Pro Glu Arg Ile Ala Pro Leu Phe Ala
271 65                  70                  75                  80
273 His Gly Ala Leu His Pro Glu Pro Ala Asp Ile Ser Val Val Glu Gly
274             85                  90                  95
276 Val Met Gly Met Phe Asp Gly Lys Leu Gly Ala Trp Pro Asp Gly Thr
277         100                 105                 110
279 Asp Asp Pro Ala Gly Phe Gly Ser Ser Ala His Ile Ala Arg Leu Leu
280         115                 120                 125
282 Asp Ala Pro Val Leu Leu Val Val Asp Gly Ser His Ser Ala Arg Thr
283         130                 135                 140
285 Ala Ala Ala Leu Cys His Gly Leu Ala Ser Tyr Asp Pro Arg Ile His
286 145                 150                 155                 160
288 Val Ala Gly Val Ile Leu Asn Arg Val Met Gly Ala Arg Val Val Asp
289             165                 170                 175
291 Glu Ile Thr Arg Gly Cys Ala Arg Val Gly Leu Pro Val Leu Gly Ala
292         180                 185                 190
294 Leu Pro Lys Ser Thr Arg Val Ala Val Gly Ser Arg His Leu Gly Leu
295         195                 200                 205
297 Val Thr Ala Asp Glu Gln Gly Asp Ala Ile Gly Ile Val Gln Gln Ala
298         210                 215                 220
300 Gly Glu Leu Val Ala Ala His Leu Asp Leu Asp Ala Ile Ala Thr Ile
301 225                 230                 235                 240
303 Ala Gly Gly Ala Pro Asp Leu Ala Val Asp Pro Trp Asp Pro Ala Ala
304             245                 250                 255
306 Glu Val Glu Pro Val Pro Gly Arg Pro Val Ile Ala Met Ala Ser Gly
307         260                 265                 270
309 Pro Ala Phe Thr Phe Arg Tyr Thr Glu Thr Ala Glu Leu Leu Glu Ala
310         275                 280                 285
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315 Pro Ala Asp Val Ser Gly Leu Tyr Leu Gly Gly Gly Phe Pro Glu Glu
316 305                 310                 315                 320
318 His Ala Glu Ala Leu Ala Gly Asn Thr Ser Leu Gly Ala Glu Ile Ala
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330 Ala Arg Ala Ala Asn Asp Ser Phe Leu Met Arg Ala Gly Glu Arg Tyr
331 385                 390                 395                 400
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VERIFICATION SUMMARY
PATENT APPLICATION: US/10/522,389

DATE: 01/26/2006
TIME: 09:19:42

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Output Set: **N:\CRF4\01262006\J522389.raw**

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